

**CLAIM AMENDMENTS**

1-31. (canceled)

32. (currently amended): A method of detecting post-transcriptional gene silencing (PTGS) of a target gene in an organism which method comprises the steps of:

analyzing-detecting in a nucleic acid extract prepared from said organism in which organism it is suspected that PTGS is occurring ~~to determine~~ the presence ~~[[or]]~~ as opposed to the absence of short RNA molecules (SRMs) which are 20-30 nucleotides in length in said extract,

characterizing any SRMs which are present in said extract ~~to determine sequence~~ wherein said characterizing comprises determining identity or similarity with said target gene,

wherein the presence of any SRMs having ~~sequence~~ identity or similarity with said target gene indicates silencing of ~~[[the]]~~ said target gene in the organism.

33. (withdrawn): The method of claim 32, wherein the organism is a plant.

34. (withdrawn): The method of claim 32, wherein the organism is a nematode.

35. (previously presented): The method of claim 32, wherein the organism is a mammal.

36. (previously presented): The method of claim 32 wherein the SRMs are short anti-sense RNA molecules (SARMs).

37. (previously presented): The method of claim 32 wherein the SRMs are short sense RNA molecules (SSRMs).

38. (canceled)

39. (previously presented): The method of claim 32, wherein the silencing of said target gene in the organism is associated with pathogen derived resistance.

40. (previously presented): The method of claim 32, wherein the silencing of said target gene in the organism is associated with modification of a specific trait by co-suppression of the target gene.

41. (currently amended): The method of claim 32, wherein the step of characterizing any SRMs present in the extract to determine ~~sequence~~ identity or similarity with a target gene is performed by a process that comprises:

tagging said SRMs with a marker, and  
preparing ~~probing~~ a library of genes from said organism, and  
identifying ~~[[those]]~~ the genes in said library ~~which share sequence identity or similarity,~~  
~~with any SRMs which are present in the extract as being genes which are silenced in the organism~~  
that bind to said SRMs whereby a gene that binds to said SRM is identified as said target gene  
which is silenced.

42-48. (canceled)

49. (currently amended): The method of claim 32, wherein said short RNA molecules are 20-25 nucleotides in length.

50-65. (canceled)

66. (new): The method of claim 32 wherein said determining identity or similarity comprises determining sequence identity or similarity.